MitoBench: An interactive visual workbench for population genetics on mitochondrial DNA



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Introduction

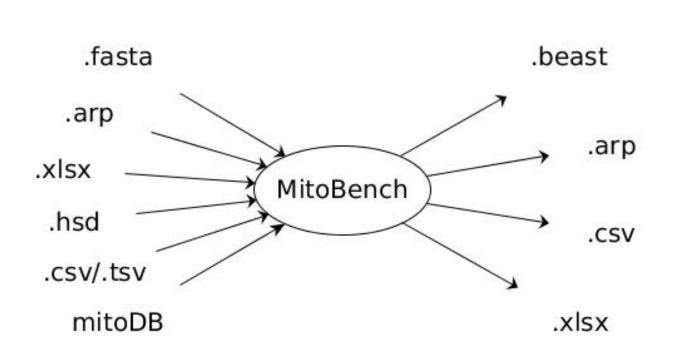
Despite the availability of modern next generation sequencing technologies and therefore nuclear human genomes, the sequencing and analysis of mitochondrial DNA (mtDNA) is still common. Especially in the research field of ancient DNA and the context of population genetics, mtDNA is often the only proxy available to study extinct populations and their relationship with modern populations. As a consequence, many population genetic studies rely on the analysis of mtDNA.

A plethora of methods for the analysis of mtDNA exist, that address questions in population genetics, phylogeny and others. However, these tools typically rely on different file formats and often require manual interaction with the data for downstream analysis. Ultimately, these steps can be cumbersome, especially for non-bioinformaticians, resulting in an increased risk of errors during the analysis.

To tackle these issues, we present MitoBench, a workbench to interactively analyze and visualize mitochondrial genomes with a focus on population genetics. The graphical user interface is kept simple, to accommodate even users without further prior knowledge on computational methods. Furthermore, it shows additional information such as metadata and statistics. Currently, MitoBench offers automatic file conversion tools to connect the workbench with existing analysis methods such as BEAST, Arlequin and others.

MitoBench

Data import and export



Data representation

ID	MTSequence	Haplogroup	Time Period	continent	country	country_region	culture_type	dating_lower
JK2880	GATCA	T1a2	Pre-Ptolemaic Period	Africa	Egypt	Beni Suef	Ancient	-669
egypt.5AJ129	GATCA	X1c	Egypt Modern	Africa	Egypt	Other	Modern	2015
egypt.6AJ68	GATCA	H3w	Egypt Modern	Africa	Egypt	Other	Modern	2015
egpg5305866	GATCA	L3f2a1	Ethiopia Modern	Africa	Ethiopia	Other	Modern	2015
egypt.6AJ63	GATCA	R0a3	Egypt Modern	Africa	Egypt	Other	Modern	2015
egpg5305863	GATCA	M1a5	Ethiopia Modern	Africa	Ethiopia	Other	Modern	2015
egpg5305862	GATCA	R0a2	Ethiopia Modern	Africa	Ethiopia	Other	Modern	2015
egpg5306038	GATCA	R0a2g	Ethiopia Modern	Africa	Ethiopia	Other	Modern	2015
egpg5306032	GATCA	L0f2b	Ethiopia Modern	Africa	Ethiopia	Other	Modern	2015
egpg5306031	GATCA	L3i2	Ethiopia Modern	Africa	Ethiopia	Other	Modern	2015
egpg5306030	GATCA	L2a1d1	Ethiopia Modern	Africa	Ethiopia	Other	Modern	2015
egypt.7AJ139	GATCA	16b	Egypt Modern	Africa	Egypt	Other	Modern	2015
JK2879	GATCA	U3b	Roman Period	Africa	Egypt	Beni Suef	Ancient	2015
JK2878	GATCA	T1a7	Ptolemaic Period	Africa	Egypt	Beni Suef	Ancient	-235
egypt.8AL34	GATCA	H20c	Egypt Modern	Africa	Egypt	Other	Modern	2015

Data grouping

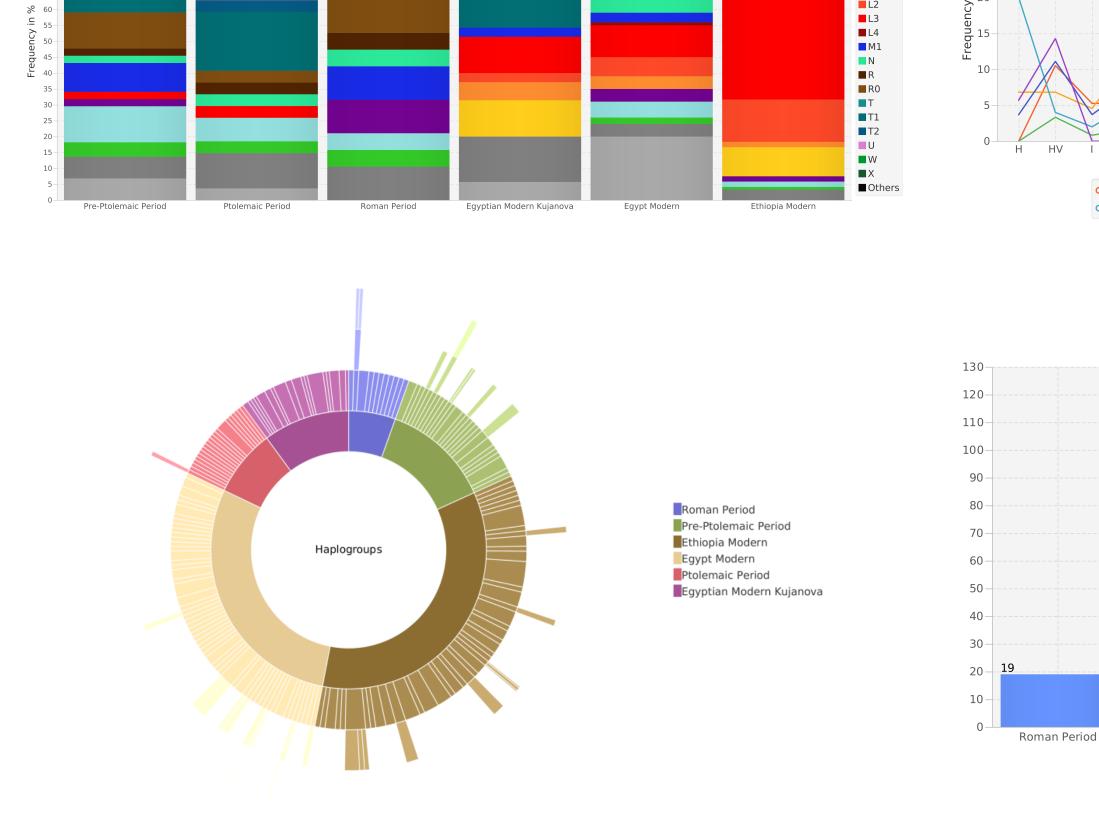
- interested in behaviour of different groups Haplogroup filtering / frequencies → Group data by feature
- internal grouping (columns not sorted)

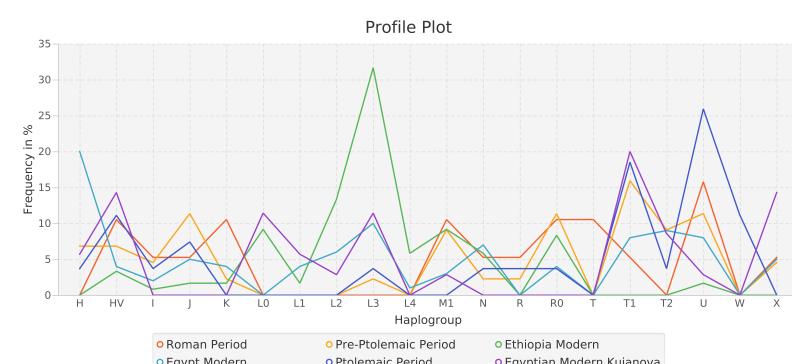
Haplogroup frequency per group

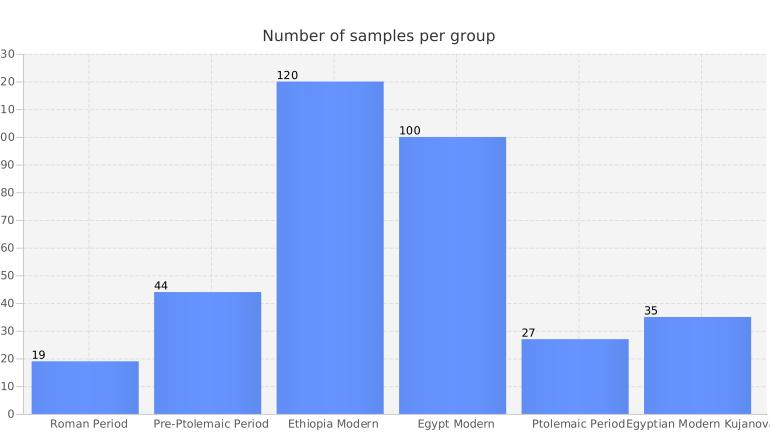
Data filtering / Statistics

- Mutation filtering / frequencies

Data visualizations







MitoDB

- Web-Frontend with Vaadin Java Framework
- Backend with PostgreSQL, providing sequence information and meta-data (SQL)
- Curated data upload with metadata
- Retrieval possible through WebUI and mitoBench

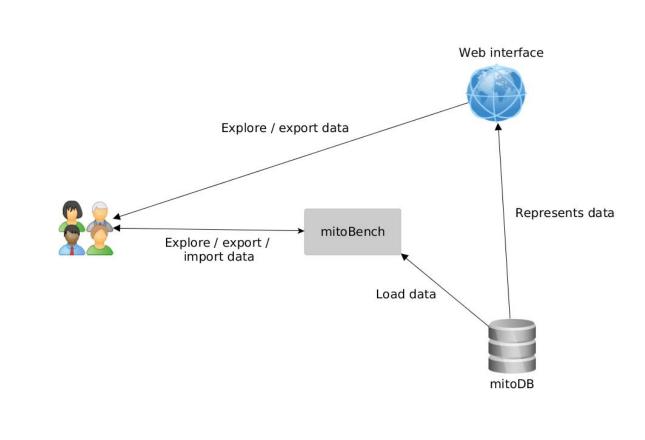
Conclusion

MitoBench

- Easy file handling and file conversion
- Combination, manipulation and visualization of mitochondrial data
- Data filtering
- Statistics

MitoDB

- Collection of mitochondrial data plus meta information
- Curated database
- accessible via mitoBench and web interface



References

- Alexei J. Drummond, et al. "Bayesian phylogenetics with BEAUti and the BEAST 1.7." Molecular biology and evolution 29.8 (2012): 1969-1973.
- Laurent Excoffier and Heidi EL Lischer. Arlequin suite ver 3.5: a new series of programs to perform population genetics analyses under linux and windows. Molecular ecology resources, 10(3):564-567, 2010.
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